

SEQUENCE LISTING

<110> FREY, Perry A.
RUZICKA, Frank J.

<120> DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE

<130> 032026/0476

<140> US 09/330,611

<141> 1999-06-11

<150> US 09/198,942

<151> 1998-11-24

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Clostridium subterminale

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| Met Ile Asn Arg Arg Tyr Glu Leu Phe Lys Asp Val Ser Asp Ala Asp | |
| 1 5 10 15 | |

| | |
|---|----|
| tgg aat gac tgg aga tgg caa gta aga aac aga ata gaa act gtt gaa | 96 |
| Trp Asn Asp Trp Arg Trp Gln Val Arg Asn Arg Ile Glu Thr Val Glu | |
| 20 25 30 | |

| | |
|---|-----|
| gaa cta aag aaa tac ata cca tta aca aaa gaa gaa gaa gga gta | 144 |
| Glu Leu Lys Lys Tyr Ile Pro Leu Thr Lys Glu Glu Gly Val | |
| 35 40 45 | |

| | |
|---|-----|
| gct caa tgt gta aaa tca tta aga atg gct att act cca tat tat cta | 192 |
| Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu | |
| 50 55 60 | |

| | |
|---|-----|
| tca tta atc gat cct aac gat cct aat gat cca gta aga aaa caa gct | 240 |
| Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala | |
| 65 70 75 80 | |

| | |
|---|-----|
| att cca aca gca tta gag ctt aac aaa gct gct gca gat ctt gaa gac | 288 |
| Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp | |
| 85 90 95 | |

| | |
|---|-----|
| cca tta cat gaa gat aca gat tca cca gta cct gga tta act cac aga | 336 |
| Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg | |
| 100 105 110 | |

| | |
|---|-----|
| tat cca gat aga gta tta tta ata act gat atg tgc tca atg tac | 384 |
| Tyr Pro Asp Arg Val Leu Leu Ile Thr Asp Met Cys Ser Met Tyr | |
| 115 120 125 | |

| | |
|---|-----|
| tgc aga cac tgt aca aga aga aga ttt gca gga caa agc gat gac tct | 432 |
| Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser | |
| 130 135 140 | |

| | | |
|---|--|------|
| atg cca atg gaa aga ata gat aaa gct ata gat tat atc aga aat act | | 480 |
| Met Pro Met Glu Arg Ile Asp Lys Ala Ile Asp Tyr Ile Arg Asn Thr | | |
| 145 150 155 160 | | |
| cct caa gtt aga gac gta tta tta tca ggt gga gac gct ctt tta gta | | 528 |
| Pro Gln Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu Val | | |
| 165 170 175 | | |
| tct gat gaa aca tta gaa tac atc ata gct aaa tta aga gaa ata cca | | 576 |
| Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro | | |
| 180 185 190 | | |
| cac gtt gaa ata gta aga ata ggt tca aga act cca gtt gtt ctt cca | | 624 |
| His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro | | |
| 195 200 205 | | |
| caa aga ata act cca gaa ctt gta aat atg ctt aaa aaa tat cat cca | | 672 |
| Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro | | |
| 210 215 220 | | |
| gta tgg tta aac act cac ttt aac cat cca aat gaa ata aca gaa gaa | | 720 |
| Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu | | |
| 225 230 235 240 | | |
| tca act aga gct tgt caa tta ctt gct gac gca gga gta cct cta gga | | 768 |
| Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly | | |
| 245 250 255 | | |
| aac caa tca gtt tta tta aga gga gtt aac gat tgc gta cac gta atg | | 816 |
| Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met | | |
| 260 265 270 | | |
| aaa gaa tta gtt aac aaa tta gta aaa ata aga gta aga gtc tac tac | | 864 |
| Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr | | |
| 275 280 285 | | |
| atc tat caa tgt gac tta tca tta gga ctt gag cac ttc aga act cca | | 912 |
| Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro | | |
| 290 295 300 | | |
| gtt tct aaa ggt atc gaa atc att gaa gga tta aga gga cat act tca | | 960 |
| Val Ser Lys Gly Ile Glu Ile Ile Glu Gly Leu Arg Gly His Thr Ser | | |
| 305 310 315 320 | | |
| gga tac tgc gta cca aca ttc gtt gtc gac gct cca ggt ggt ggt gga | | 1008 |
| Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly | | |
| 325 330 335 | | |
| aaa aca cca gtt atg cca aac tac gtt att tca caa agt cat gac aaa | | 1056 |
| Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys | | |
| 340 345 350 | | |
| gta ata tta aga aac ttt gaa ggt gtt ata aca act tat tca gaa cca | | 1104 |
| Val Ile Leu Arg Asn Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro | | |
| 355 360 365 | | |
| ata aac tat act cca gga tgc aac tgt gat gtt tgc act ggc aag aaa | | 1152 |
| Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys | | |
| 370 375 380 | | |
| aaa gtt cat aag gtt gga gtt gct gga tta tta aac gga gaa gga atg | | 1200 |
| Lys Val His Lys Val Gly Val Ala Gly Leu Leu Asn Gly Glu Gly Met | | |
| 385 390 395 400 | | |

gct cta gaa cca gta gga tta gag aga aat aag aga cac gtt caa gaa 1248
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1251

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Glu Leu Lys Tyr Ile Pro Leu Thr Lys Glu Glu Glu Gly Val
35 40 45

Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu
50 55 60

Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala
65 70 75 80

Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp
85 90 95

Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg
100 105 110

Tyr Pro Asp Arg Val Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
115 120 125

Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser
130 135 140

Met Pro Met Glu Arg Ile Asp Lys Ala Ile Asp Tyr Ile Arg Asn Thr
145 150 155 160

Pro Gln Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu Val
165 170 175

Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro
180 185 190

His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro
195 200 205

Gin Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro
210 215 220

Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu
225 230 235 240

Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly
245 250 255

Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met
260 265 270

Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr
275 280 285

Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro
290 295 300

Val Ser Lys Gly Ile Glu Ile Ile Glu Gly Leu Arg Gly His Thr Ser
305 310 315 320

Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly
325 330 335

Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys
340 345 350

Val Ile Leu Arg Asn Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro
355 360 365

Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys
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Lys Val His Lys Val Gly Val Ala Gly Leu Leu Asn Gly Glu Gly Met
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Thr Gln Leu Ala Asp Val Val Thr Asp Pro Asp Glu Leu Leu Arg Leu
20 25 30

ttg aat ata gac gcg gag gaa aaa ctg tta gcc gga cgc agc gcc aaa 144
Leu Asn Ile Asp Ala Glu Glu Lys Leu Ala Gly Arg Ser Ala Lys
35 40 45

aag ctt ttt gcc ctg cgt gtg ccc cgc tca ttt atc gat cgc atg gag 192
Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu
50 55 60

aaa ggc aat ccg gac gat cct ctt ttg cgt cag gta ctt acc tcg caa 240
Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln
65 70 75 80 95

gat gag ttt gtc atc gcg ccc gga ttc tcc acc gac cca ctg gaa gaa 288
Asp Glu Phe Val Ile Ala Pro Gly Phe Ser Thr Asp Pro Leu Glu Glu
85 90 95

| | |
|--|------|
| cag cac agc gta gtg cct ggt ttg cat aaa tac cac aac cgg gcg Gln His Ser Val Val Pro Gly Leu Leu His Lys Tyr His Asn Arg Ala | 336 |
| 100 105 110 | |
| ctt ttg ctg gtc aaa ggc ggc tgc gcg gta aat tgc cgc tat tgc ttc Leu Leu Leu Val Lys Gly Gly Cys Ala Val Asn Cys Arg Tyr Cys Phe | 384 |
| 115 120 125 | |
| cgt cgt cac ttc ccc tat gcc gaa aat gag ggc aac aag cgt aac tgg Arg Arg His Phe Pro Tyr Ala Glu Asn Gln Gly Asn Lys Arg Asn Trp | 432 |
| 130 135 140 | |
| caa act gca ctt gag tat gtt gct gcg cat ccg gaa ctg gac gag atg Gln Thr Ala Leu Glu Tyr Val Ala Ala His Pro Glu Leu Asp Glu Met | 480 |
| 145 150 155 160 | |
| att ttc tcc ggc ggc gat ccg ctg atg gcg aaa gat cac gag ctg gac Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu Asp | 528 |
| 165 170 175 | |
| tgg ttg ctc aca caa ctg gaa gcc atc ccg cat ata aaa cgt ctg cgg Trp Leu Leu Gln Leu Glu Ala Ile Pro His Ile Lys Arg Leu Arg | 576 |
| 180 185 190 | |
| att cac agc cgt ctg ccg att gtg atc ccg gca cgt atc acc gag gcg Ile His Ser Arg Leu Pro Ile Val Ile Pro Ala Arg Ile Thr Glu Ala | 624 |
| 195 200 205 | |
| ctg gtt gaa tgc ttt gcc cgt tct acg ctg caa atc ttg ctg gtc aat Leu Val Glu Cys Phe Ala Arg Ser Thr Leu Gln Ile Leu Leu Val Asn | 672 |
| 210 215 220 | |
| cac atc aac cat gcc aat gag gta gat gaa aca ttc cgt cag gcg atg His Ile Asn His Ala Asn Glu Val Asp Glu Thr Phe Arg Gln Ala Met | 720 |
| 225 230 235 240 | |
| gct aag ttg cgc cgg gta ggc gtt act ttg ctg aac cag agc gtt ctg Ala Lys Leu Arg Arg Val Gly Val Thr Leu Leu Asn Gln Ser Val Leu | 768 |
| 245 250 255 | |
| tta cgt gat gtg aac gat aac gca caa acc ctg gca aac ctg agt aat Leu Arg Asp Val Asn Asp Asn Ala Gln Thr Leu Ala Asn Leu Ser Asn | 816 |
| 260 265 270 | |
| gcg ttg ttc gat gcc ggc gta atg ccg tat tac ctg cat gtg ctc gat Ala Leu Phe Asp Ala Gly Val Met Pro Tyr Tyr Leu His Val Leu Asp | 864 |
| 275 280 285 | |
| aaa gta cag ggc gcg gcg cat ttt atg gtg agt gat gac gaa gca cgg Lys Val Gln Gly Ala Ala His Phe Met Val Ser Asp Asp Glu Ala Arg | 912 |
| 290 295 300 | |
| cag att atg cgt gag ttg ctg aca ctg gtg tcg gga tat ctg gtg ccg Gln Ile Met Arg Glu Leu Leu Thr Leu Val Ser Gly Tyr Leu Val Pro | 960 |
| 305 310 315 320 | |
| aaa ctg gcg cga gaa att ggc ggc gaa ccc agc aaa acg ccg ctg gat Lys Leu Ala Arg Glu Ile Gly Gly Glu Pro Ser Lys Thr Pro Leu Asp | 1008 |
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| ctc cag cta cgc cag cag taa Leu Gln Leu Arg Gln Gln | 1029 |
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35 40 45
Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu
50 55 60
Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln
65 70 75 80
Asp Glu Phe Val Ile Ala Pro Gly Phe Ser Thr Asp Pro Leu Glu Glu
85 90 95
Gln His Ser Val Val Pro Gly Leu Leu His Lys Tyr His Asn Arg Ala
100 105 110
Leu Leu Leu Val Lys Gly Gly Cys Ala Val Asn Cys Arg Tyr Cys Phe
115 120 125
Arg Arg His Phe Pro Tyr Ala Glu Asn Gln Gly Asn Lys Arg Asn Trp
130 135 140
Gln Thr Ala Leu Glu Tyr Val Ala Ala His Pro Glu Leu Asp Glu Met
145 150 155 160
Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu Asp
165 170 175
Trp Leu Leu Thr Gln Leu Glu Ala Ile Pro His Ile Lys Arg Leu Arg
180 185 190
Ile His Ser Arg Leu Pro Ile Val Ile Pro Ala Arg Ile Thr Glu Ala
195 200 205
Leu Val Glu Cys Phe Ala Arg Ser Thr Leu Gln Ile Leu Leu Val Asn
210 215 220
His Ile Asn His Ala Asn Glu Val Asp Glu Thr Phe Arg Gln Ala Met
225 230 235 240
Ala Lys Leu Arg Arg Val Gly Val Thr Leu Leu Asn Gln Ser Val Leu
245 250 255
Leu Arg Asp Val Asn Asp Asn Ala Gln Thr Leu Ala Asn Leu Ser Asn
260 265 270
Ala Leu Phe Asp Ala Gly Val Met Pro Tyr Tyr Leu His Val Leu Asp
275 280 285
Lys Val Gln Gly Ala Ala His Phe Met Val Ser Asp Asp Glu Ala Arg
290 295 300

Gln Ile Met Arg Glu Leu Leu Thr Leu Val Ser Gly Tyr Leu Val Pro
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Lys Leu Ala Arg Glu Ile Gly Gly Pro Ser Lys Thr Pro Leu Asp
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Leu Gln Leu Arg Gln Gln
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ctc aca att cta aaa aat gcc att tca gat cct aaa tta tta cta aaa 96
Leu Thr Ile Leu Lys Asn Ala Ile Ser Asp Pro Lys Leu Leu Lys
20 25 30

gcc tta aat tta cca gaa gat gat ttt gag caa tcc att gct gcg cgg 144
Ala Leu Asn Leu Pro Glu Asp Asp Phe Glu Gln Ser Ile Ala Ala Arg
35 40 45

aaa ctt ttt tcg ctc cgc gtg cca caa cct ttc att gat aaa ata gaa 192
Lys Leu Phe Ser Leu Arg Val Pro Gln Pro Phe Ile Asp Lys Ile Glu
50 55 60

aaa ggt aat ccg caa gat ccc ctt ttc ttg caa gtg atg tgt tct gat 240
Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp
65 70 75 80

tta gag ttt gtg caa gcg gag gga ttt agt acg gat ccc tta gaa gaa 288
Leu Glu Phe Val Gln Ala Glu Gly Phe Ser Thr Asp Pro Leu Glu Glu
85 90 95

aaa aat gcc aat gcg gtg cca aat att ctt cat aaa tat aga aat cgc 336
Lys Asn Ala Asn Ala Val Pro Asn Ile Leu His Lys Tyr Arg Asn Arg
100 105 110

ttg etc ttt atg gca aaa ggc ggt tgt gcg gtg aat tgt cgt tat tgc 384
Leu Leu Phe Met Ala Lys Gly Gly Cys Ala Val Asn Cys Arg Tyr Cys
115 120 125

ttt cgc cga cat ttt cct tac gat gaa aac cca gga aat aaa aaa agc 432
Phe Arg Arg His Phe Pro Tyr Asp Glu Asn Pro Gly Asn Lys Lys Ser
130 135 140

tgg caa ctg gcg tta gat tac att gcg gca cat tct gaa ata gaa gaa 480
Trp Gln Leu Ala Leu Asp Tyr Ile Ala Ala His Ser Glu Ile Glu Glu
145 150 155 160

gtg att ttt tca ggt ggc gat cct tta atg gca aat gac cac gaa tta 528
Val Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu
165 170 175

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|------|-----|-----|---|------|---|------|---|------|---|-----|---|-----|---|------|---|------|---|------|---|-----|---|-----|---|-----|---|------|---|------|---|-----|---|-----|---|-----|---|------|---|------|---|-----|---|-----|---|-----|---|------|---|------|---|-----|---|-----|---|-----|---|------|---|------|---|-----|---|-----|---|-----|---|------|---|------|---|-----|---|-----|---|------|---|------|---------|-----|-----|-----|---|------|---|------|---------|-----|-----|-----|-----|--|-------------|------|---------|--|
| gcg tgg tta ata aaa cat ttg gaa aat ata ccg cac tta caa cgt ttg | 576 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala Trp Leu Ile Lys His Leu Glu Asn Ile Pro His Leu Gln Arg Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 180 | 185 | 185 | 190 | cgt att cac acc cgt ttg cct gtt gtg att ccg caa ccg att act gat | 624 | Arg Ile His Thr Arg Leu Pro Val Val Ile Pro Gln Arg Ile Thr Asp | | 195 | 200 | 200 | 205 | gaa ttt tgc act tta tta gca gaa act cgt ttg caa aca gtt atg gtg | 672 | Glu Phe Cys Thr Leu Leu Ala Glu Thr Arg Leu Gln Thr Val Met Val | | 210 | 215 | 215 | 220 | aca cac att aat cac ccg aat gaa att gat caa att ttt gct cat gcg | 720 | Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala | | 225 | 230 | 230 | 235 | 235 | 240 | atg caa aaa tta aac gcc gtg aat gtc acg ctt ttg aat caa tct gtt | 768 | Met Gln Lys Leu Asn Ala Val Asn Val Thr Leu Asn Gln Ser Val | | 245 | 250 | 250 | 255 | 255 | | ttg cta aaa ggc gtg aat gat gat ggc caa att cta aaa ata ttg agc | 816 | Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | 260 | 265 | 265 | 270 | 270 | | gat aaa ctt ttt caa aca ggc att ttg cct tat tac ttg cat ttg ctg | 864 | Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | 275 | 280 | 280 | 285 | 285 | | gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | 290 | 295 | 295 | 300 | 300 | | atg caa atc tat aaa acc ttg caa tct ctg act tct ggc tat ctt gtt | 960 | Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | |
| 185 | 190 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| cgt att cac acc cgt ttg cct gtt gtg att ccg caa ccg att act gat | 624 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arg Ile His Thr Arg Leu Pro Val Val Ile Pro Gln Arg Ile Thr Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 195 | 200 | 200 | 205 | gaa ttt tgc act tta tta gca gaa act cgt ttg caa aca gtt atg gtg | 672 | Glu Phe Cys Thr Leu Leu Ala Glu Thr Arg Leu Gln Thr Val Met Val | | 210 | 215 | 215 | 220 | aca cac att aat cac ccg aat gaa att gat caa att ttt gct cat gcg | 720 | Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala | | 225 | 230 | 230 | 235 | 235 | 240 | atg caa aaa tta aac gcc gtg aat gtc acg ctt ttg aat caa tct gtt | 768 | Met Gln Lys Leu Asn Ala Val Asn Val Thr Leu Asn Gln Ser Val | | 245 | 250 | 250 | 255 | 255 | | ttg cta aaa ggc gtg aat gat gat ggc caa att cta aaa ata ttg agc | 816 | Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | 260 | 265 | 265 | 270 | 270 | | gat aaa ctt ttt caa aca ggc att ttg cct tat tac ttg cat ttg ctg | 864 | Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | 275 | 280 | 280 | 285 | 285 | | gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | 290 | 295 | 295 | 300 | 300 | | atg caa atc tat aaa acc ttg caa tct ctg act tct ggc tat ctt gtt | 960 | Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | | | | | | | | | |
| 200 | 205 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gaa ttt tgc act tta tta gca gaa act cgt ttg caa aca gtt atg gtg | 672 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu Phe Cys Thr Leu Leu Ala Glu Thr Arg Leu Gln Thr Val Met Val | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 210 | 215 | 215 | 220 | aca cac att aat cac ccg aat gaa att gat caa att ttt gct cat gcg | 720 | Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala | | 225 | 230 | 230 | 235 | 235 | 240 | atg caa aaa tta aac gcc gtg aat gtc acg ctt ttg aat caa tct gtt | 768 | Met Gln Lys Leu Asn Ala Val Asn Val Thr Leu Asn Gln Ser Val | | 245 | 250 | 250 | 255 | 255 | | ttg cta aaa ggc gtg aat gat gat ggc caa att cta aaa ata ttg agc | 816 | Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | 260 | 265 | 265 | 270 | 270 | | gat aaa ctt ttt caa aca ggc att ttg cct tat tac ttg cat ttg ctg | 864 | Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | 275 | 280 | 280 | 285 | 285 | | gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | 290 | 295 | 295 | 300 | 300 | | atg caa atc tat aaa acc ttg caa tct ctg act tct ggc tat ctt gtt | 960 | Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | | | | | | | | | | | | | | | | | |
| 215 | 220 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aca cac att aat cac ccg aat gaa att gat caa att ttt gct cat gcg | 720 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 225 | 230 | 230 | 235 | 235 | 240 | atg caa aaa tta aac gcc gtg aat gtc acg ctt ttg aat caa tct gtt | 768 | Met Gln Lys Leu Asn Ala Val Asn Val Thr Leu Asn Gln Ser Val | | 245 | 250 | 250 | 255 | 255 | | ttg cta aaa ggc gtg aat gat gat ggc caa att cta aaa ata ttg agc | 816 | Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | 260 | 265 | 265 | 270 | 270 | | gat aaa ctt ttt caa aca ggc att ttg cct tat tac ttg cat ttg ctg | 864 | Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | 275 | 280 | 280 | 285 | 285 | | gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | 290 | 295 | 295 | 300 | 300 | | atg caa atc tat aaa acc ttg caa tct ctg act tct ggc tat ctt gtt | 960 | Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | | | | | | | | | | | | | | | | | | | | | | | | | |
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| atg caa aaa tta aac gcc gtg aat gtc acg ctt ttg aat caa tct gtt | 768 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Met Gln Lys Leu Asn Ala Val Asn Val Thr Leu Asn Gln Ser Val | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 245 | 250 | 250 | 255 | 255 | | ttg cta aaa ggc gtg aat gat gat ggc caa att cta aaa ata ttg agc | 816 | Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | 260 | 265 | 265 | 270 | 270 | | gat aaa ctt ttt caa aca ggc att ttg cct tat tac ttg cat ttg ctg | 864 | Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | 275 | 280 | 280 | 285 | 285 | | gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | 290 | 295 | 295 | 300 | 300 | | atg caa atc tat aaa acc ttg caa tct ctg act tct ggc tat ctt gtt | 960 | Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 250 | 255 | 255 | | ttg cta aaa ggc gtg aat gat gat ggc caa att cta aaa ata ttg agc | 816 | Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | 260 | 265 | 265 | 270 | 270 | | gat aaa ctt ttt caa aca ggc att ttg cct tat tac ttg cat ttg ctg | 864 | Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | 275 | 280 | 280 | 285 | 285 | | gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | 290 | 295 | 295 | 300 | 300 | | atg caa atc tat aaa acc ttg caa tct ctg act tct ggc tat ctt gtt | 960 | Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| gat aaa gtt caa ggg ggc agc cat ttt ttg att agc gat att gaa gct | 912 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 300 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 305 | 310 | 310 | 315 | 315 | 320 | 320 | | cct aaa ctt gca cga gaa att gcg ggc gag cca aat aag act tta tac | 1008 | Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | 325 | 330 | 330 | 335 | 335 | | gca gaa taa | 1017 | Ala Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 320 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 335 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gca gaa taa | 1017 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

<210> 6
<211> 338
<212> PRT
<213> Haemophilus influenzae

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| <400> 6 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Met Arg Ile Leu Pro Gln Glu Pro Val Ile Arg Glu Glu Gln Asn Trp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1 | 5 | 5 | 10 | 10 | 15 | Leu Thr Ile Leu Lys Asn Ala Ile Ser Asp Pro Lys Leu Leu Lys | | 20 | 25 | 25 | 30 | Ala Leu Asn Leu Pro Glu Asp Asp Phe Glu Gln Ser Ile Ala Ala Arg | | 35 | 40 | 40 | 45 | Lys Leu Phe Ser Leu Arg Val Pro Gln Pro Phe Ile Asp Lys Ile Glu | | 50 | 55 | 55 | 60 | Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp | | 65 | 70 | 70 | 75 | 75 | 80 |
| 5 | 10 | 10 | 15 | Leu Thr Ile Leu Lys Asn Ala Ile Ser Asp Pro Lys Leu Leu Lys | | 20 | 25 | 25 | 30 | Ala Leu Asn Leu Pro Glu Asp Asp Phe Glu Gln Ser Ile Ala Ala Arg | | 35 | 40 | 40 | 45 | Lys Leu Phe Ser Leu Arg Val Pro Gln Pro Phe Ile Asp Lys Ile Glu | | 50 | 55 | 55 | 60 | Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp | | 65 | 70 | 70 | 75 | 75 | 80 | | |
| 10 | 15 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Leu Thr Ile Leu Lys Asn Ala Ile Ser Asp Pro Lys Leu Leu Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 20 | 25 | 25 | 30 | Ala Leu Asn Leu Pro Glu Asp Asp Phe Glu Gln Ser Ile Ala Ala Arg | | 35 | 40 | 40 | 45 | Lys Leu Phe Ser Leu Arg Val Pro Gln Pro Phe Ile Asp Lys Ile Glu | | 50 | 55 | 55 | 60 | Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp | | 65 | 70 | 70 | 75 | 75 | 80 | | | | | | | | |
| 25 | 30 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala Leu Asn Leu Pro Glu Asp Asp Phe Glu Gln Ser Ile Ala Ala Arg | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 35 | 40 | 40 | 45 | Lys Leu Phe Ser Leu Arg Val Pro Gln Pro Phe Ile Asp Lys Ile Glu | | 50 | 55 | 55 | 60 | Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp | | 65 | 70 | 70 | 75 | 75 | 80 | | | | | | | | | | | | | | |
| 40 | 45 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys Leu Phe Ser Leu Arg Val Pro Gln Pro Phe Ile Asp Lys Ile Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 50 | 55 | 55 | 60 | Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp | | 65 | 70 | 70 | 75 | 75 | 80 | | | | | | | | | | | | | | | | | | | | |
| 55 | 60 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 65 | 70 | 70 | 75 | 75 | 80 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 70 | 75 | 75 | 80 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 75 | 80 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Leu Glu Phe Val Gln Ala Glu Gly Phe Ser Thr Asp Pro Leu Glu Glu
85 90 95

Lys Asn Ala Asn Ala Val Pro Asn Ile Leu His Lys Tyr Arg Asn Arg
100 105 110

Leu Leu Phe Met Ala Lys Gly Gly Cys Ala Val Asn Cys Arg Tyr Cys
115 120 125

Phe Arg Arg His Phe Pro Tyr Asp Glu Asn Pro Gly Asn Lys Lys Ser
130 135 140

Trp Gln Leu Ala Leu Asp Tyr Ile Ala Ala His Ser Glu Ile Glu Glu
145 150 155 160

Val Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu
165 170 175

Ala Trp Leu Ile Lys His Leu Glu Asn Ile Pro His Leu Gln Arg Leu
180 185 190

Arg Ile His Thr Arg Leu Pro Val Val Ile Pro Gln Arg Ile Thr Asp
195 200 205

Glu Phe Cys Thr Leu Leu Ala Glu Thr Arg Leu Gln Thr Val Met Val
210 215 220

Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala
225 230 235 240

Met Gln Lys Leu Asn Ala Val Asn Val Thr Leu Leu Asn Gln Ser Val
245 250 255

Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser
260 265 270

Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu
275 280 285

Asp Lys Val Gln Gly Ala Ser His Phe Leu Ile Ser Asp Ile Glu Ala
290 295 300

Met Gln Ile Tyr Lys Thr Leu Gln Ser Leu Thr Ser Gly Tyr Leu Val
305 310 315 320

Pro Lys Leu Ala Arg Glu Ile Ala Gly Glu Pro Asn Lys Thr Leu Tyr
325 330 335

Ala Glu

<210> 7

<211> 1251

<212> DNA

<213> Porphyromonas gingivalis

<220>

<221> CDS

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Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
1 5 10 15

caa tgg aac gac tgg cat tgg caq gtc ctc aat cga att gag acg ctc 96
Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gaa gag gga 144
Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
35 40 45

gta aaa gaa tgg ctc aaa gta ctc cga atg gct atc aca cct tat tat 192
Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
50 55 60

ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa 240
Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
65 70 75 80

gcc att cct act cat gag aac ctg gta cgt gct cct gaa gat cag gta 288
Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
85 90 95

gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat 336
Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
100 105 110

cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg 384
Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
115 120 125

tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct 432
Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
130 135 140

tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat 480
Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
145 150 155 160

aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ett 528
Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
165 170 175

gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata 576
Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
180 185 190

cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctt 624
Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
195 200 205

cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat 672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Tyr His
210 215 220

ccg gtg tgg ctg aac act cac ttc aac cac ccc aat gaa gtt acc gaa 720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
225 230 235 240

gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg 768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
245 250 255

ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg 816
Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
260 265 270

atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac 864
Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
275 280 285

tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg 912
Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
290 295 300

ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc 960
Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr
305 310 315 320

tcg ggc tat get gtt cct acc ttt gtg gta gat gct ccg ggg ggt ggt 1008
Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly
325 330 335

ggt aag ata cct gta atg ccg aac tat gtt gta tct cag tcc cca cga 1056
Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
340 345 350

cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag 1104
His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
355 360 365

ccg gag aat tat cat gag gag tgt gat tgt gag gac tgt cga gcc ggt 1152
Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
370 375 380

aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct 1200
Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gln Gln Leu Ala
385 390 395 400

atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac 1248
Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
405 410 415

tga 1251

<210> 8
<211> 416
<212> PRT
<213> Porphyromonas gingivalis

<400> 8
Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
1 5 10 15

Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
35 40 45

Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
65 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly
325 330 335

Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
405 410 415

<210> 9
<211> 1416
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1413)

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Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
1 5 10 15

tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96
Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
20 25 30

ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192
Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240
Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
65 70 75 80

ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288
Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
85 90 95

cac aaa aca aaa tac gat ctg gaa gac ccg ctt cat gag gat gaa gat 336
His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp
100 105 110

tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384
Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
115 120 125

ctt gtc acg aat caa tgt tcc atg tac tgc cgc tac tgc aca aga agg 432
Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

ccg ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480
Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta 528
Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

att tca ggc ggt gat ggg ctg ctc att aac gac caa att tta gaa tat 576
Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc 624
Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

| | | | |
|---|---------|------|-----|
| gga aca aga gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg | | 672 | |
| Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu | | | |
| 210 . 215 | 220 | | |
| tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt | | 720 | |
| Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe | | | |
| 225 230 | 235 240 | | |
| aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag | | 768 | |
| Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys | | | |
| 245 | 250 | 255 | |
| ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca | | 816 | |
| Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala | | | |
| 260 | 265 | 270 | |
| ggt att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg | | 864 | |
| Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu | | | |
| 275 | 280 | 285 | |
| gta aaa act aga gtc cgt cct tat tat att tac caa ttt gat ctg tca | | 912 | |
| Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser | | | |
| 290 | 295 | 300 | |
| gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc | | 960 | |
| Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile | | | |
| 305 | 310 | 315 | 320 |
| att gaa ggg ctg aga ggt cat acc tca ggc tat ggc gtt cct acc ttt | | 1008 | |
| Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe | | | |
| 325 | 330 | 335 | |
| gtc gtt gac gca cca ggc gga gga ggt aaa atc gcc ctg cag cca aac | | 1056 | |
| Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn | | | |
| 340 | 345 | 350 | |
| tat gtc ctg tca caa agt cct gac aaa gtc atc tta aga aat ttt gaa | | 1104 | |
| Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu | | | |
| 355 | 360 | 365 | |
| ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag | | 1152 | |
| Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln | | | |
| 370 | 375 | 380 | |
| gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag | | 1200 | |
| Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys | | | |
| 385 | 390 | 395 | 400 |
| gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt | | 1248 | |
| Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe | | | |
| 405 | 410 | 415 | |
| aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca | | 1296 | |
| Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala | | | |
| 420 | 425 | 430 | |
| aat ccg gag cat gaa aca tta aaa gat ccg cgt gag aaa aga gat cag | | 1344 | |
| Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln | | | |
| 435 | 440 | 445 | |
| ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act | | 1392 | |
| Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr | | | |
| 450 | 455 | 460 | |

gaa tgc gga ggg gat tct tca tga
Glu Cys Gly Gly Asp Ser Ser
465 470

1416

<210> 10
<211> 471
<212> PRT
<213> Bacillus subtilis

<400> 10
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1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
85 90 95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp
100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
115 120 125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
450 455 460

Glu Cys Gly Gly Asp Ser Ser
465 470

<210> 11
<211> 1188
<212> DNA
<213> Deinococcus radiodurans

<220>
<221> CDS
<222> (1)..(1188)

<400> 11
tgg caa ggc gta ccc gag gag cag tgg tac gag tgg aaa tgg cag ctc 48
Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu
1 5 10 15

aag aac cgc atc aac agt gtg gag gag ttg cag gaa gtc ctg acc ctc 96
Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu
20 25 30

acc gag tcc gag tac cgg ggt gcg tcc gcc gag ggc att ttc cgc ctc 144
Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu
35 40 45

gac atc acg ccg tat ttc gcg tcc ctc atg gag ccc gaa gac ccc acc 192
Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr
50 55 60

| | | |
|---|--|-----|
| tgc ccg gtg cgc cgt cag gtg att ccc acc gag gag gag ctc cag ccg | | 240 |
| Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro | | |
| 65 70 75 80 | | |
| ttc acc tcc atg atg gaa gac tac tct ctc cgc gag gat aag cac tcg ccc | | 288 |
| Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro | | |
| 85 90 95 | | |
| gtg ccg ggg ctg gtg cac cgc tac ccc gac cgc gtg ctg atg ctg gtc | | 336 |
| Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val | | |
| 100 105 110 | | |
| acg acc cag tgc cgc agc tac tgc cgc tac tgc acc cga agc cgc atc | | 384 |
| Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile | | |
| 115 120 125 | | |
| gtg ggc gac ccc acc gag acg ttc aat ccc gcc gag tat gag ggc cag | | 432 |
| Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln | | |
| 130 135 140 | | |
| ctc aac tac ctg cgc aac acc ccg cag gtg cgc gac gtg ctg ctt tcc | | 480 |
| Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser | | |
| 145 150 155 160 | | |
| ggc ggc gac ccc aca ctc cgc ccg aag gtg ctg ggg cgc ctg ctt | | 528 |
| Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu | | |
| 165 170 175 | | |
| tcc gaa ctt cgt aaa atc gag cac atc gaa atc atc cgc atc ggc acc | | 576 |
| Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr | | |
| 180 185 190 | | |
| cgc gtg ccc gtg ttc atg ccc atg cgc gtg acc cag gaa ctg tgc gac | | 624 |
| Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp | | |
| 195 200 205 | | |
| acg ctc gcc gaa cac cat ccg ctg tgg atg aac att cac gtc aac cac | | 672 |
| Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His | | |
| 210 215 220 | | |
| ccc aag gaa atc acc ccc gaa gtg gcc gag ggc tgt gac cgt ctg acc | | 720 |
| Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr | | |
| 225 230 235 240 | | |
| cgc gcg ggc gtg ccg ctc gcc aac gag agc gtg ctg ctg cgc ggc gtg | | 768 |
| Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val | | |
| 245 250 255 | | |
| aac gac cac ccg gtc atc atg caa aag ctg ctg cgc gag ctc gtc aaa | | 816 |
| Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys | | |
| 260 265 270 | | |
| att cgg gtg cgc ccc tac tac tac tac cag tgc gac ctc gtg cac ggc | | 864 |
| Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly | | |
| 275 280 285 | | |
| gct ggg cac ctg cgc acc acg gtc agt aag ggt ctg gaa atc atg gaa | | 912 |
| Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu | | |
| 290 295 300 | | |
| tcc ctg cgc ggc cac acc tcc ggc tac agc gtg ccc acc tac gtg gtg | | 960 |
| Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val | | |
| 305 310 315 320 | | |

gac gcg ccc ggc ggc ggc aag att ccg gtg ggc ccc aac tac gtg 1008
Asp Ala Pro Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val
325 330 335

ctc tcg cac agc cct gag aag ctg att ctg cgc aac ttc gag ggc tac 1056
Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr
340 345 350

atc gcc ggc tac tcg gag ccc acc gat tac acc ggc ccc gac atg ggc 1104
Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala
355 360 365

att cct gac gac tgg att cgc aag gaa ccc ggc cag acc ggc atc ttc 1152
Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe
370 375 380

ggc ctg atg gaa ggc gag cgc att tcc atc gag ccg 1188
Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro
385 390 395

<210> 12

<211> 396

<212> PRT

<213> Deinococcus radiodurans

<400> 12

Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu
1 5 10 15

Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu
20 25 30

Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu
35 40 45

Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr
50 55 60

Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro
65 70 75 80

Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro
85 90 95

Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val
100 105 110

Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile
115 120 125

Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln
130 135 140

Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser
145 150 155 160

Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu
165 170 175

Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr
180 185 190

Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp
195 200 205

Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His
210 215 220

Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr
225 230 235 240

Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val
245 250 255

Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys
260 265 270

Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly
275 280 285

Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu
290 295 300

Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val
305 310 315 320

Asp Ala Pro Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val
325 330 335

Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr
340 345 350

Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala
355 360 365

Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe
370 375 380

Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro
385 390 395

<210> 13
<211> 1113
<212> DNA
<213> Aquifex aeolicus

<220>
<221> CDS
<222> (1)..(1110)

<400> 13
atg cgt cgc ttt ttt gag aat gta ccg gaa aac ctc tgg agg agc tac 48
Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr
1 5 10 15

gag tgg cag ata caa aac agg ata aaa act ctt aag gag ata aaa aag 96
Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys
20 25 30

tac tta aaa ctc ctt ccc gag gag gaa gaa gga att aaa aga act caa 144
Tyr Leu Lys Leu Leu Pro Glu Glu Glu Gly Ile Lys Arg Thr Gln
35 40 45

| | | |
|---|--|-----|
| ggg ctt tat ccc ttt ggc ata aca cct tac tac ctc tct tta ata aat | | 192 |
| Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn | | |
| 50 55 60 | | |
| cca gag gac ccg aag gat cct ata aga ctt cag gca atc ccc cgc gtt | | 240 |
| Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val | | |
| 65 70 75 80 | | |
| gta gaa gtt gat gaa aag gtt cag tct gcg gga gaa cca gac gct ctg | | 288 |
| Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu | | |
| 85 90 95 | | |
| aaa gaa gaa gga gat att ccg ggt ctt aca cac agg tat ccc gac agg | | 336 |
| Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg | | |
| 100 105 110 | | |
| gtt ctt tta aac gtc act acc ttt tgt gcg gtt tac tgc agg cac tgt | | 384 |
| Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys | | |
| 115 120 125 | | |
| atg aga aag agg ata ttc tct cag ggt gag agg gca agg act aaa gag | | 432 |
| Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu | | |
| 130 135 140 | | |
| gaa ata gac acg atg att gat tac ata aag aga cac gaa gag ata agg | | 480 |
| Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg | | |
| 145 150 155 160 | | |
| gat gtc tta att tca ggt ggt gag cca ctt tcc ctt tcc ttg gaa aaa | | 528 |
| Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys | | |
| 165 170 175 | | |
| ctt gaa tac tta ctc tca agg tta agg gaa ata aaa cac gtg gaa att | | 576 |
| Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile | | |
| 180 185 190 | | |
| ata cgc ttt ggg acg agg ctt ccc gtt ctt gca ccc cag agg ttc ttt | | 624 |
| Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe | | |
| 195 200 205 | | |
| aac gat aaa ctt ctg gac ata ctg gaa aaa tac tcc ccc ata tgg ata | | 672 |
| Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile | | |
| 210 215 220 | | |
| aac act cac ttc aac cat ccg aat gag ata acc gag tac gcg gaa gaa | | 720 |
| Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu | | |
| 225 230 235 240 | | |
| gcg gtg gac agg ctc ctg aga agg ggc att ccc gtg aac aac cag aca | | 768 |
| Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr | | |
| 245 250 255 | | |
| gtc cta ctt aaa ggc gta aac gac gac cct gaa gtt atg cta aaa ctc | | 816 |
| Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu | | |
| 260 265 270 | | |
| ttt aga aaa ctt tta agg ata aag gta aag ccc cag tac ctc ttt cac | | 864 |
| Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His | | |
| 275 280 285 | | |
| tgc gac ccg ata aag gga gcg gtt cac ttt agg act acg ata gac aaa | | 912 |
| Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys | | |
| 290 295 300 | | |

gga ctt gaa ata atg aga tat ttg agg gga agg ctg agc ggt ttc ggg 960
Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly
305 310 315 320

ata ccc act tac gcg gtg gac ctc ccg gga ggg aaa ggt aag gtt cct 1008
Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro
325 330 335

ctt ctt ccc aac tac gta aag aaa agg aaa ggt aat aag ttc tgg ttt 1056
Leu Leu Pro Asn Tyr Val Lys Arg Lys Gly Asn Lys Lys Trp Phe
340 345 350

gaa agt ttc acg ggt gag gtc gta gaa tac gaa gta acg gaa gta tgg 1104
Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp
355 360 365

gaa cct tga 1113
Glu Pro
370

<210> 14

<211> 370

<212> PRT

<213> Aquifex aeolicus

<400> 14

Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr
1 5 10 15

Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys
20 25 30

Tyr Leu Lys Leu Leu Pro Glu Glu Glu Gly Ile Lys Arg Thr Gln
35 40 45

Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn
50 55 60

Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val
65 70 75 80

Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu
85 90 95

Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg
100 105 110

Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys
115 120 125

Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu
130 135 140

Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg
145 150 155 160

Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys
165 170 175

Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile
180 185 190

Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe
195 200 205

Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile
210 215 220

Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu
225 230 235 240

Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr
245 250 255

Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu
260 265 270

Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His
275 280 285

Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys
290 295 300

Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly
305 310 315 320

Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro
325 330 335

Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe
340 345 350

Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp
355 360 365

Glu Pro
370

<210> 15

<211> 1065

<212> DNA

<213> Treponema pallidum

<220>
<221> CDS
<222> (1)..(1065)

<400> 15
atg tct atg gct gag tgg acc cgg gaa cag aga aag aga cga ggt gca
Met Ser Met Aia Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala
1 5 10 15

ggg cgt gct gat gag cat tgg cgg acg ttg agt cct gcc tct tgc gcg
Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala
20 25 30

gca gat gcg ctg acg gag cat att tcc cca gcg tat gcg cat tta att
Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile
35 40 45

gca caa gcg cag ggc gcg gac gcg cag gcg ctg aaa cgt cag gtg tgc
Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys
50 55 60

| | |
|---|-----|
| ttt gcg cca cag gag cgt gtg gtg cat gct tgc gag tgg gcc gac cca Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro 65 70 75 80 | 240 |
| ttg ggt gag gac cgg tac tgc gtg aca ccc ttt ttg gtg cat cag tat Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr 85 90 95 | 288 |
| gcg aat cgt gtg ttg aca gga cgt tgc ttt tca cac tgt Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys 100 105 110 | 336 |
| cgc tat tgt ttt cgc cgc ggt ttc atc gcc caa cgt gca ggg tgg atc Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile 115 120 125 | 384 |
| ccc aac gaa gag cgc gag aag att att acg tat ctt cgt gct acc cct Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro 130 135 140 | 432 |
| tcg gtg aag gaa atc ctg gtt tca ggt ggt gat cca ctc act ggt tct Ser Val Lys Glu Ile Val Ser Gly Gly Asp Pro Leu Thr Gly Ser 145 150 155 160 | 480 |
| ttt gca cag gtc aca tcg ctt ttc cgc gca ctg cgc agt gta gcg cgg Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro 165 170 175 | 528 |
| gat ttg att att cgt ctg tgc act cgc gca gtc acc ttt gct ccg cag Asp Leu Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln 180 185 190 | 576 |
| gcc ttt act ccc gag ctg att gcg ttt ctg cag gag atg aag ccg gtg Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val 195 200 205 | 624 |
| tgg ata att ccg cat att aat cac ccg gca gag ctc ggt tct acg cag Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln 210 215 220 | 672 |
| ccg gcg ctc gag gcc tgc gta ggc gca ggc ctc cct gtc caa tcg Arg Ala Val Leu Glu Ala Cys Val Gly Ala Leu Pro Val Gln Ser 225 230 235 240 | 720 |
| cag tcg gta ctg ttg cgc ggg gtc aac gat tcg gta gag acg ctg tgc Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys 245 250 255 | 768 |
| aca ctg ttt cac gcg ctc act tgt ctg ggg gtt aag ccg ggg tat cta Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu 260 265 270 | 816 |
| ttt cag ttg gat ttg gcg cct gga act ggg gat ttt cgt gtg cca ctt Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu 275 280 285 | 864 |
| tct gac acg cta gct ctg tgg cgc aca ttg aag gag cgc ctc tca ggg Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly 290 295 300 | 912 |
| ttg tcg ctt ccc acg ctt gcg gtc gac ttg cca ggg ggt gga aag Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Lys 305 310 315 320 | 960 |

ttt ccg ctt gtg gca ttg gcc cag caa gat gtc acc tgg cat cag 1008
Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln
325 330 335

gaa cgc gag gcg ttc tcc gca cgc ggc atc gat ggc gcg tgg tac acg 1056
Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr
340 345 350

tac ccg ttc 1065
Tyr Pro Phe
355

<210> 16
<211> 355
<212> PRT
<213> Treponema pallidum

<400> 16
Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala
1 5 10 15

Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala
20 25 30

Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile
35 40 45

Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys
50 55 60

Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro
65 70 75 80

Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr
85 90 95

Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys
100 105 110

Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile
115 120 125

Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro
130 135 140

Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser
145 150 155 160

Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro
165 170 175

Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln
180 185 190

Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val
195 200 205

Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln
210 215 220

Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser
225 230 235 240

Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys
245 250 255

Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu
260 265 270

Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu
275 280 285

Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly
290 295 300

Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Lys
305 310 315 320

Phe Pro Leu Val Ala Leu Ala Gln Gln Asp Val Thr Trp His Gln
325 330 335

Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr
340 345 350

Tyr Pro Phe
355

<210> 17
<211> 6
<212> PRT
<213> Clostridium subterminale

<400> 17
Lys Asp Val Ser Asp Ala
1 5

<210> 18
<211> 17
<212> DNA
<213> Clostridium subterminale

<220>
<221> modified_base
<222> (9)
<223> n is inosine

<220>
<221> modified_base
<222> (12)
<223> n is inosine

<400> 18
aargaygtnw sngaygc 17

<210> 19
<211> 6
<212> PRT
<213> Clostridium subterminale

<400> 19
Gln Ser His Asp Lys Val
1 5

<210> 20
<211> 20
<212> DNA
<213> Clostridium subterminale

<220>
<221> modified_base
<222> (3)
<223> n is inosine

<220>
<221> modified_base
<222> (15)
<223> n is inosine

<400> 20
atnacyttrt crtgnswytg

20

<210> 21
<211> 48
<212> PRT
<213> Clostridium subterminale

<400> 21
Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys Val Ile Leu Arg Asn
1 5 10 15

Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro Ile Asn Tyr Thr Pro
20 25 30

Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys Lys Val His Lys Val
35 40 45

<210> 22
<211> 15
<212> PRT
<213> Clostridium subterminale

<400> 22
Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln
1 5 10 15

<210> 23
<211> 16
<212> PRT
<213> Clostridium subterminale

<400> 23
Met Ile Asn Arg Arg Tyr Glu Leu Phe Lys Asp Val Ser Asp Ala Asp
1 5 10 15

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 24
atcctaacga tcctaatgat cc 22

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 25
tggatggta aagtgagtg 19

<210> 26
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Probe

<400> 26
atcctaacga tcctaatgat ccagtaagaa aacaaggctat tccaacagca tttagagctta 60
acaaaggctgc tgcatatccatttt gaaagaccat tacatgaaga tacagattca ccagtagctg 120
gattaaactca cagatatcca gatacgatgtt tattataat aactgtatgt tgctcaatgt 180
actgcagaca ctgtacaaaaga agaaggatgg caggacaaag cgatgactct atgccatgg 240
aaagaataga taaagctata gattatataca gaaataactcc tcaagttaga gacgtattat 300
tatcagggtgg agacgcttctt ttagtatctg atgaaacatt agaatacatac atagctaaat 360
taagagaaaat accacacgtt gaaatagtaa gaataggttc aagaactcca gttgttcttc 420
cacaagaat aactccagaa ctgtaaaata tgctaaaaa atatcatcca gtatggtaa 480
acactcaactt taaccatcca 500

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 27
tacacatatg ataaatagaa gatatg 26

<210> 28
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 28
tagactcgag ttattcttga acgtgtctc 29

<210> 29
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 29
tacagaatcc atgataaaata gaagatatg 29

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 30
tagaaaagctt ttattcttga acgtgtctc 29

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 31
tataggatcc gaccgtataa ttcacgcgt tacacc 36

<210> 32
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 32
tagagaatcc gattcagtca ggcgtcccat tatac 34